

Description

Recombinant Microorganism

Technical Field

The present invention relates to a recombinant microorganism which may be used to produce useful proteins or polypeptides, as well as to such proteins and polypeptides.

Technical Background

Microorganisms are widely used for industrially producing a broad range of useful substances, including alcoholic beverages, certain types of foods such as *miso* and *shoyu*, amino acids, organic acids, nucleic-acid-related substances, antibiotics, sugars, lipids, and proteins. These substances also find diversified uses, including foods, pharmaceuticals, detergents, products for daily use such as cosmetics, and a variety of chemical raw materials.

In industrial production of useful substances by use of microorganisms, improvement of productivity is one major topic of interest, and one approach therefor is breeding of microorganisms through mutagenesis or other genetic means. Recently, in particular, with advancement of microbial genetics and biotechnology, more efficient breeding of useful microorganisms is performed through gene recombination techniques, and in association therewith, host microorganisms for obtaining recombinant genes are under development. For example, *Bacillus subtilis* Marburg No. 168, which has already

been confirmed to be safe and have excellent characteristics as a host microorganism, has been further improved.

However, microorganisms inherently possess diversified genes so that they can cope with environmental changes in the natural world, and thus, they do not necessarily exhibit high production efficiency of proteins or similar substances in industrial production, where only limited production media are employed.

Disclosure of the Invention

The present invention provides a recombinant microorganism prepared by transferring, to a mutant strain of microorganism from which at least one gene participating in membrane permeation of maltose (particularly either *glvR* or *glvC*) or one or more genes functionally equivalent to the gene have been deleted or knocked out, a gene encoding a heterologous protein or polypeptide.

Brief Description of the Drawing

Fig. 1 schematically shows a method for preparing a DNA fragment for deleting a gene through SOE-PCR (SOE: splicing by overlap extension) (see Gene, 77, 61 (1989), and a method for deleting a target gene (replacing the target gene with a drug resistance gene) through use of the DNA.

Modes for Carrying out the Invention

The present invention is directed to a recombinant

microorganism obtained by transferring, into a host microorganism which is capable of producing protein or polypeptide with increased productivity and which was identified by the present inventors, a gene encoding a protein or polypeptide, and to a method for producing a protein or polypeptide by use of the recombinant microorganism.

The present inventors have conducted extensive studies on, among many different genes encoded on the genome of a microorganism, genes which are not needed in or which are detrimental to the production of useful proteins or polypeptides, and surprisingly, have found that, when a gene encoding a target protein or polypeptide is transferred to a microorganism after a specific gene participating in membrane permeation of maltose employed as a predominant carbon source of a culture medium or a gene functionally equivalent to the gene is deleted or knocked out from the genome of the microorganism, productivity of the target protein or polypeptide is enhanced as compared with the case before the deletion or knocking out.

By use of the recombinant microorganism of the present invention, a target protein or polypeptide can be produced on a large scale with high efficiency.

In the present invention, homology between amino acid sequences and that between nucleic acid sequences are both determined by use of the Lipman-Pearson method (Science, 227, 1435 (1985)). Specifically, calculation is performed by use

of a homology analysis program (Search Homology) developed by genetic information processing software, Genetyx-Win (Software Development Co., Ltd.), with ktup (the unit size to be compared) being set 2.

No particular limitation is imposed on a parent microorganism for constructing the microorganism of the present invention, so long as it has a gene participating in membrane permeation of maltose. Specifically, any of the *Bacillus subtilis* genes or genes functionally equivalent thereto as shown in Table 1 may be employed. When culture is performed by use of a medium containing maltose or maltooligo-saccharide as a primary carbon source, the microorganism is preferably of another class having a different maltose permeation system in which the mentioned gene does not participate. The gene may be of wild-type or a mutant. Specific examples include *Bacillus subtilis* and similar microorganisms belonging to the genus *Bacillus*, microorganisms belonging to the genus *Clostridium*, and yeast. *Inter alia*, microorganisms belonging to the genus *Bacillus* are preferred. In particular, *Bacillus subtilis* is preferred, from the viewpoint that complete genomic information of this microorganism has already been obtained, and thus genetic engineering techniques and genomic engineering techniques have been established, and that the microorganism has ability to secrete the produced protein extracellularly.

Examples of the target protein or polypeptide to be produced by use of the microorganism of the present invention

include enzymes, physiologically active substances, and other proteins and polypeptides which find utility in foods, pharmaceuticals, cosmetics, detergents, fiber treating agents, clinical assay agents, etc.

In the present invention, genes which are to be deleted or knocked out are those participating in membrane permeation of maltose. These genes are any of the *Bacillus subtilis* genes shown in Table 1, or are selected from among the genes functionally equivalent thereto.

The names, numbers, and functions of respective genes in the Tables contained herein conform with the *Bacillus subtilis* genome data reported in Nature, 390, 249-256 (1997) and made public by JAFAN (Japan Functional Analysis Network for *Bacillus subtilis*; BSORF DB) on the Internet (<http://bacillus.genome.ad.jp/>, renewed June 17, 2003).

Table 1

Name of the gene	Gene ID	Functions or other information of the gene
<i>glvC</i>	BG11848	PTS maltose-specific enzyme IICB
<i>glvR</i>	BG11847	Positive regulator for <i>glvARC</i> operon

Genes originating from other microorganisms, preferably from bacteria belonging to the genus *Bacillus*, which have the same functions as any of the *Bacillus subtilis* genes shown in Table 1, or have 70% or more homology with the nucleotide sequence of any of the genes shown in Table 1, preferably 80% or more homology, more preferably 90% or more, further

preferably 95% or more, yet more preferably 98% or more, should be interpreted to be functionally equivalent to the genes shown in Table 1, and thus to constitute the genes which are to be deleted or knocked out according to the present invention.

The aforementioned genes participate in membrane permeation of maltose during incorporation thereof into cells; i.e., phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS, J. Mol. Microbiol. Biotechnol., 4, 37, 2002). Specifically, the genes include a *glvC* gene encoding maltose-specific permease IICB involved in PTS; a *glvR* gene encoding a positive regulator for a *glv* operon containing the *glvC* gene; and genes functionally equivalent thereto. If any of the aforementioned genes is deleted or knocked out, maltose membrane permeability of cells is conceivably reduced. However, surprisingly, the present inventors have now found that use of a host microorganism in which any of the genes is deleted or knocked out through enzyme-producing culture employing a medium containing maltose as a predominant carbon source achieves a remarkable enhancement in productivity of protein as compared with the use of a conventional host microorganism.

Incidentally, a *ptsH* gene (BG10200) and a *ptsI* gene (BG10201) have also been known to participate in uptake of maltose in cells via PTS. Therefore, deletion or knocking out of any of *ptsH* and *ptsI* is predicted to effectively enhance productivity of protein. Thus, if a regulator gene

glcT gene (BG12593), which is required for expression of a *pts* operon including the above two genes, is deleted or knocked out, productivity of protein should be enhanced.

An alternative method for achieving the present invention is inactivation, or knocking out, of a target gene by inserting thereto a DNA fragment of another origin or introducing a mutation to the transcription/translation-initiation region of the gene. Preferably, however, the target genes are physically deleted. The number of gene(s) to be deleted or knocked out is one or more, and two or more genes may be deleted. When a microorganism of the present invention is constructed, deletion or inactivation of a gene or genes other than those participated in membrane permeation of maltose is possible. In such a case, a more improved effect is expected.

In an example procedure for deleting or knocking out the genes, any of the target genes shown in Table 1 is deleted or knocked out according to a plan which has been set up in advance. Alternatively, randomized deletion of genes or mutation by way of knocking out is performed, followed by evaluation on protein productivity and gene analysis.

The target gene may be deleted or knocked out through homologous recombination. That is, a DNA fragment containing a portion of the target gene is cloned with an appropriate plasmid vector to thereby obtain a circular recombinant plasmid, and the resultant plasmid is transferred into cells of a parent microorganism. Thereafter, through homologous

recombination effected in a partial region of the target gene, the target gene on the genome of the parent microorganism is cleaved, thereby completing inactivation of the target gene. Alternatively, the target gene is mutated (or knocked out) by substitution or insertion of a base, or a linear DNA fragment containing a region outside the target gene sequence but not containing the target gene may be constituted through PCR or a similar method, and the thus-engineered gene or fragment is transferred into a cell of a parent microorganism. At two sites outside the mutation within the target gene in the genome of the parent microorganism genome, or at two regions outside the target gene sequence, double crossing-over homologous recombination is caused to occur, to thereby attain substitution with a gene fragment in which the target gene on the genome is deleted or knocked out.

Particularly when the parent microorganism used to construct the microorganism of the present invention is *Bacillus subtilis*, since several reports have already described methods for deleting or knocking out the target gene (see, for example, Mol. Gen. Genet., 223, 268 1990), repetition of any of such methods may be followed, to thereby produce a host microorganism of the present invention.

Randomized gene deletion or inactivation may be performed through use of a method similar to the above-described method for inducing homologous recombination by use of a randomly cloned DNA fragment, or by way of irradiation of a parent microorganism with gamma rays or similar rays.

Next will be described in more detail a deletion method employing double crossing over by use of a DNA fragment designed for the deletion purpose, the DNA fragment being prepared through SOE-PCR (Gene, 77, 61, 1989). However, in the present invention, the method for deleting genes is not limited to only the below-described method.

The DNA fragment use for the deletion purpose is a fragment constructed such that a drug resistant marker gene is inserted between a ca. 0.2 to 3 kb upstream sequence which flanks and is upstream of the gene to be deleted, and a ca. 0.2 to 3 kb downstream sequence which flanks and is downstream of the same gene. In the first cycle of PCR, the following three fragments are prepared: the upstream and the downstream fragments, which are to be deleted, and the drug resistant marker gene. The primers to be used in this step may, for example, be those specifically designed so that an upstream 10-30 base pair sequence of a drug resistance gene is added to the lower end of the upstream fragment, and a downstream 10-30 base pair sequence of the drug resistance marker gene is added to the upper end of the downstream fragment (Fig. 1).

Next, using three PCR fragments prepared in the first cycle as templates, the second cycle of PCR is performed by use of an upper primer of the upstream fragment and a lower primer of the downstream fragment (out-side primers). This step causes annealing with the drug resistance marker gene fragment in the sequence of the above-engineered drug

resistance marker gene, and through PCR amplification, there can be obtained a DNA fragment with the drug resistance marker gene inserted between the upstream fragment and the downstream fragment (Fig. 1).

When a chloramphenicol-resistant gene is employed as a drug resistance marker gene, a DNA fragment for deleting a gene can be obtained through SOE-PCR under typical conditions described in literature (see, for example, PCR Protocols. Current Methods and Applications, Edited by B. A. White, Humana Press, pp. 251 (1993), Gene, 77, 61, 1989), by use of an appropriate template DNA and a primer set such as that shown in Table 2 and a conventional enzyme kit for PCR (e.g., Pyrobest DNA Polymerase (product of Takara Shuzo)).

When the thus-obtained DNA fragment for effecting gene deletion is introduced into cells through the competent method or a similar method, intracellular genetic recombination occurs in homologous regions which are present upstream and downstream of the gene to be deleted. Thus, cells in which the target gene has been substituted by a drug resistance gene can be selectively separated through employment of a drug resistance marker (Fig. 1).

Specifically, when a DNA fragment for gene deletion prepared by use of a primer set shown in Table 2 is introduced into cells, colonies which have grown on an agar culture medium containing chloramphenicol are separated, and deletion of the target gene by way of substitution by the chloramphenicol-resistant gene is confirmed through an appropriate method

such as PCR employing a genome as a template.

Subsequently, when a gene encoding a target protein or polypeptide is transferred to a host mutant microorganism strain from which any of the *Bacillus subtilis* genes shown in Table 1, or one or more genes selected from among the genes corresponding thereto has been deleted or knocked out, the microorganism of the present invention can be obtained.

No particular limitation is imposed on the gene encoding the target protein or polypeptide. Examples of the protein and polypeptide include physiologically-active peptides and enzymes for industrial purposes such as detergents, foods, fibers, feeds, chemicals, medicine, and diagnostic agents. Industrial enzymes may be functionally grouped into oxidoreductases, transferases, hydrolases, lyases, isomerases, and ligases/synthetases. Preferably, hydrolases such as cellulase, α -amylase, and protease may be used. Specific examples include cellulase belonging to family 5 in the classification of hydrolase (Bioche M. J., 280, 309, 1991); in particular, cellulase derived from a microorganism, more particularly cellulase derived from the genus *Bacillus*. Other specific examples of the types of industrial enzymes include alkaline cellulase which is derived from the genus *Bacillus* and has an amino-acid SEQ ID NOs: 2 or 4, alkaline cellulase which has an amino-acid sequence in which one or more amino acid(s) has been deleted, substituted, or added, and cellulase which has an another amino-acid sequence having 70% homology with said amino-acid

sequence, preferably 80% homology, more preferably 90%, further preferably 95%, particularly preferably 98% or more.

Specific examples of α -amylase include α -amylase derived from a microorganism, preferably liquefied amylase derived from the genus *Bacillus*. More specific examples include alkaline amylase which is derived from the genus *Bacillus* and has an amino-acid sequence of SEQ ID NO: 22, and amylase which has another amino-acid sequence having 70% homology with said amino-acid sequence, preferably 80% homology, more preferably 90%, further preferably 95%, particularly preferably 98% or more. The homology of the amino-acid sequence is calculated by the Lipman-Pearson method (Science, 227, 1435 (1985)). Specific examples of protease include serine protease and metalloprotease which are derived from microorganisms, particularly those belonging to the genus *Bacillus*.

Specific examples of protease include serine protease and metallo-protease which are derived from microorganisms, preferably those belonging to the genus *Bacillus*.

Preferably, a gene coding for a target protein or polypeptide has, on its upstream region thereof, one or more regulatory regions relating to transcription, translation, or secretion of the gene (specially, one or more regions selected from among a transcription initiation regulatory region including a promoter and a transcription initiation site; a translation initiation region including a ribosome-binding site and a start codon; and a secretion signal

peptide region) properly ligated thereto. Preferably, it is preferred that three regions consisting of the transcription initiation regulatory region, the translation initiation regulatory region, and the secretion signal region be ligated to the target gene. Further preferably, the secretion signal peptide region is one that originates from the cellulase gene of a microorganism belonging to the genus *Bacillus*, and the transcription initiation region and the translation initiation region is a 0.6 to 1 kb region upstream of the cellulase gene. In one preferred example, a transcription initiation regulatory region, a translation initiation region, and a secretion signal peptide region of a cellulase gene derived from a microorganism belonging to the genus *Bacillus* disclosed in, for example, Japanese Patent Application Laid-Open (*kokai*) Nos. 2000-210081 and 190793/1990; i.e., a cellulase gene derived from KSM-S237 strain (FERM BP-7875) or KSM-64 strain (FERM BP-2886), is properly ligated to a structural gene of the target protein or polypeptide. More specifically, preferred DNA fragments to be ligated include a nucleotide sequence of base numbers 1 to 659 of SEQ ID NO: 1; a nucleotide sequence of base numbers 1 to 696 of a cellulase gene of SEQ ID NO: 3; a DNA fragment having a nucleotide sequence having 70% homology with any one of said nucleotide sequences, preferably 80% homology, more preferably 90%, further preferably 95%, particularly preferably 98% or more; or a DNA fragment having a nucleotide sequence lacking a portion of any one of said nucleotide sequences. Preferably,

one of these DNA fragments is properly ligated to a structural gene of the target protein or polypeptide. As used herein, a DNA fragment having a nucleotide sequence lacking a portion of any one of the above-mentioned nucleotide sequences is intended to mean a DNA fragment which has functions relating to transcription, translation, and secretion of the gene, without having a portion of any one of the above-mentioned nucleotide sequences.

The recombinant microorganism of the present invention can be obtained by a conventional transformation technique in which a recombinant plasmid containing a DNA fragment which includes a gene encoding the target protein or polypeptide, and is ligated to a proper plasmid vector is transferred into a host microorganism cell. Alternatively, the recombinant microorganism may be obtained making use of a DNA fragment prepared by ligating the above DNA fragment to a proper region which is homologous with a certain portion of the host microorganism genome, and inserted directly into a host microorganism genome.

The target protein or polypeptide obtained by use of the recombinant microorganism of the present invention may be produced in such a manner that a corresponding cell strain is inoculated onto a culture medium containing assimilable carbon sources and nitrogen sources, and other essential components; the cell strain is cultured through a conventional microorganism culturing method; and subsequently, protein or polypeptide is collected and purified. No

particular limitation is imposed on the ingredients and composition of a culture medium, and the medium preferably contains maltose or maltooligo saccharide as a carbon source so as to perform satisfactory culturing.

Through the aforementioned procedure, a host mutant microorganism strain in which any of the *Bacillus subtilis* genes shown in Table 1 or one or more genes selected from genes functionally equivalent thereto have been deleted or knocked out can be engineered. In addition, by use of such a mutant strain, a recombinant microorganism can be produced. Thus, a useful protein or polypeptide can be effectively produced through employment of the mutant strain or the recombinant microorganism.

Working example of the method for constructing a recombinant strain belonging to *Bacillus subtilis* from which the *glvC* gene (BG11848) or *glvR* gene (BG11847) of *Bacillus subtilis* has been deleted, and the method for producing cellulase and α -amylase by use of the recombinant microorganism will next be described in detail.

Examples

Example 1

A genome DNA sample, serving as a template, extracted from *Bacillus subtilis* 168 strain and two primer sets (*glvC*-AF and *glvC*-A/CmR; and *glvC*-B/CmF and *glvC*-BR) shown in Table 2 were used to prepare a 0.5 kb fragment (A) flanking the upstream side of the *glvC* gene on the genome and a 0.5 kb fragment (B) flanking the downstream side of the *glvC* gene.

A recombinant plasmid pC194 (J. Bacteriol. 150 (2), 815 (1982)) serving as a template and a primer set formed of glvC-A/CmF and glvC-B/CmR shown in Table 2 were used to prepare a 0.9 kb fragment (C) containing the chloramphenicol-resistant gene. Subsequently, SOE-PCR was performed by use of the primers glvC-AF and glvC-BR shown in Table 2, and by use of the thus-prepared three fragments (A), (B), and (C) in combination as templates, a 1.9 kb DNA fragment in which the fragments (A), (B), and (C) were ligated in this sequence was prepared (see Fig. 1). By use of the thus-prepared DNA fragment, *Bacillus subtilis* 168 strain was transformed through the competent method. Colonies grown in an LB agar medium containing chloramphenicol were collected as transformants. The genome of the above-obtained transformant was extracted, and PCR performed thereon confirmed that the *glvC* gene had been deleted and substituted by a chloramphenicol-resistant gene.

Table 2

Primer	Nucleotide sequence	SEQ ID NO:
glvC-AF	AAATGCGCAAAAGATATGCGC	5
glvC-A/CmR	CTAATGGGTGCTTTAGTTGCTGATACCGACGATAATGCC	6
glvC-B/CmF	CTGCCCCGTTAGTTGAAGAGACTGCCCTCCTTTTCGG	7
glvC-BR	CGCAAACTCATAAAAATCATATTT	8
glvC-A/CmF	CAACTAAAGCACCCATTAGTTCAACA	9
glvC-B/CmR	CTTCAACTAACGGGGCAGGTTAGTGAC	10
glvR-AF	CAGATGATATGGTGAAAAAATCAAATCCG	11
glvR-A/CmR	GTTATCCGCTCACAATTCCGAGCTGCATATCAGATCCC	12

glvR-B/CmF	CGTCGTGACTGGGAAAACTGTTGATTACAAAGAGGCAG	13
glvR-BR	CCATCGGCCAAATATAAGACACAGCCAACGC	14
glvR-A/CmF	GAATTGTGAGCGGATAAC	15
glvR-B/CmR	GTTTTCCCAGTCACGACG	16
glcT-AF	ATAATGCCCGCTTCCCAACC	17
glcT-A/CmR	GTTATCCGCTCACAATTCGGATCCTCAGCTCCTTTGTC	18
glcT-B/CmF	CGTCGTGACTGGGAAAACTCATCTGATACCGATTAACC	19
glcT-BR	CAACTGAATCCGAAGGAATG	20

Example 2

In a manner similar to that of Example 1, two primer sets (glvR-AF and glvR-A/CmR; and glvR-B/CmF and glvR-BR) shown in Table 2 were used to prepare a 0.6 kb fragment (A) flanking the upstream side of the *glvR* gene on the genome and a 0.6 kb fragment (B) flanking the downstream side of the *glvR* gene. A chloramphenicol-resistant gene of plasmid pC194 (J. Bacteriol. 150 (2), 815 (1982)) was inserted into the XbaI-BamHI cleavage site of plasmid pUC18, to thereby prepare a recombinant plasmid pCBB 31. The recombinant plasmid pCBB31 serving as a template and a primer set formed of glvR-A/CmF and glvR-B/CmR shown in Table 2 were used to prepare a 0.9 kb fragment (C) containing the chloramphenicol-resistant gene. Subsequently, SOE-PCR was performed by use of the primers glvR-AF and glvR-BR shown in Table 2, and by use of the thus-prepared three fragments (A), (B), and (C) in combination as templates, a 2.2 kb DNA fragment in which the fragments (A), (B), and (C) were ligated in this sequence was prepared (see Fig. 1). By use of the thus-prepared DNA fragment, *Bacillus subtilis* 168 strain was transformed

through the competent method. Colonies grown in an LB agar medium containing chloramphenicol were collected as transformants. The genome of the above-obtained transformant was extracted, and PCR performed thereon confirmed that the *glvR* gene had been deleted and substituted by a chloramphenicol-resistant gene. In a similar manner, a transformant in which the *glcT* gene had been deleted and substituted by a chloramphenicol-resistant gene was isolated by use of two primer sets (*glcT*-AF and *glcT*-A/CmR; and *glcT*-B/CmF and *glcT*-BR).

Example 3

To each of the gene-deleted strains obtained in Examples 1 and 2 and to *Bacillus subtilis* 168 strain serving as a control, a recombinant plasmid pHY-S237 was introduced through the protoplast transformation method. The recombinant plasmid pHY-S237 was prepared by inserting a DNA fragment (3.1 kb) encoding an alkaline cellulase derived from *Bacillus* sp. KSM-S237 strain (SEQ ID NO: 1, Japanese Patent Application Laid-Open (*kokai*) No. 2000-210081) into the restriction enzyme *Bam*HI cleavage site of a shuttle vector pHY300 PLK. Each of the thus-obtained cell strains was shake-cultured in an LB medium (5 mL) overnight at 30°C. The culture broth (0.03 mL) was inoculated to a 2 × L-maltose medium (2% tryptone, 1% yeast extract, 1% NaCl, 7.5% maltose, 7.5 ppm manganese sulfate 4-5 hydrate, and 15 ppm tetracycline), followed by shake culturing at 30°C for three days. After completion of culturing, cells were removed

through centrifugation, and alkaline cellulase activity of the supernatant obtained from the culture was determined, thereby calculating the amount of the alkaline cellulase secreted from the cells during culturing; i.e., the amount of the extracellularly produced alkaline cellulase. As is clear from Table 3, more effective production, or secretion, of alkaline cellulase has been confirmed in all cases where a gene-deleted spore-formable strain was employed as a host, as compared with the control 168 strain (wild type strain).

Table 3

Name of deleted gene	Gene ID	Gene size (bp)	Size of deleted fragment (bp)	Amount of produced (secreted) alkaline cellulase (relative value)
<i>glvC</i>	BG11848	1584	1498	161
<i>glvR</i>	BG11847	715	765	140
<i>glcT</i>	BG12593	858	811	110
None (Wild type)	—	—	—	100

Example 4

To each of the gene-deleted strains obtained in Examples 1 to 3 and to *Bacillus subtilis* 168 strain serving as a control, recombinant plasmid pHSP-K38 was introduced through the protoplast transformation method. The recombinant plasmid pHSP-K38 was prepared by inserting, into the restriction enzyme *BagII*-*XbaI* cleavage site of a shuttle vector pHY300 PLK, a 2.1 kb fragment (SEQ ID No: 21) prepared by ligating an upstream 0.6 kb fragment (SEQ ID NO: 3) including portions of a promoter region and a signal sequence region of an alkaline cellulase gene with an upstream side of a DNA fragment (1.5 kb) encoding a mature enzyme region

(Asp1-Gln480) of an alkaline amylase gene derived from *Bacillus* sp. KSM-K38 strain (Japanese Patent Application Laid-Open (*kokai*) No. 2000-184882, Eur. J. Biochem., 268, 2974 (2001)). Each of the thus-obtained cell strains was shake-cultured in an LB medium (5 mL) overnight at 30°C. The culture broth (0.03 mL) was inoculated to a 2 × L-maltose medium (2% tryptone, 1% yeast extract, 1% NaCl, 7.5% maltose, 7.5 ppm manganese sulfate 4-5 hydrate, and 15 ppm tetracycline), followed by shake culturing at 30°C for three to six days. After completion of culturing, cells were removed through centrifugation, and alkaline amylase activity of the supernatant obtained from the culture was determined, thereby calculating the amount of the alkaline amylase secreted from the cells during culturing; i.e., the amount of the extracellularly produced alkaline amylase. As is clear from Table 4, more effective production, or secretion, of alkaline amylase has been confirmed in the case where a gene-deleted strain was employed as a host, as compared with the control 168 strain (wild type strain).

Table 4

Name of deleted gene	Gene ID	Gene size (bp)	Size of deleted fragment (bp)	Amount of produced (secreted) alkaline amylase (relative value)
<i>glvC</i>	BG11848	1584	1498	202
<i>glvR</i>	BG11847	715	765	153
None (Wild type)	—	—	—	100